sequence of a target nucleic acid to be analyzed on the basis of a value of 4^n which correspond to all of the n unit sequences formed of n nucleotide sequences, wherein n is an integer of 2 or more;

(b) a first extraction step of extracting a sequence having p number of nucleotides and present on the nucleotide sequence of a target nucleic acid, said p is larger than n by m, wherein m is an integer of 1 or more;

(c) a second calculation step of extracting n unit sequences occurring on the candidate sequence extracted in the first extraction step and obtaining an occurrence frequency index of the candidate sequence on the nucleotide sequence of the target nucleic acid on the basis of the occurrence frequency of each of the n unit sequences obtained in the first calculation step; and

(d) a second extraction step of selecting a single or a plurality of candidate sequences, each of the candidate sequences having a low occurrence frequency index based on a threshold value of the occurrence frequency index obtained from the second calculation step, wherein the lower the occurrence frequency index, the higher the specificity.

A2 Cont'd

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8. (Amended) The method according to claim 6, further comprising a third extraction step of selecting a candidate sequence having a low stability of a molecular secondary structure which is not capable of forming a stable secondary structure and whereby a sequence which is capable of readily hybridizing with a target nucleic acid under hybridization conditions is selected.

A3

9. (Amended) The method according to claim 8, wherein the stability of the molecular secondary structure is determined by at least one property selected from the group consisting of (i) thermal stability as measured by a value of Tm and (ii) stability of an intramolecular secondary structure.

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11. (Amended) The method according to any one of claims 6 to 10, wherein all of the calculations involved in steps (a) to (d) are sequentially performed by a computer.

12. (Amended) The method according to any one of claims 6 to 10, wherein said nucleotide sequence of an analytical oligo nucleic acid is used in (i) a PCR method for detecting a specific nucleotide sequence present in a nucleotide sequence of a nucleic acid by using an enzyme reaction which requires hybridization reactions of a nucleic acid, or (ii) in a hybridization reaction of a nucleic acid employing a probe.

Please cancel claims 1 ~~to~~ 5, without prejudice.